

Greedy Forward Regression for Variable Screening¹

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Abstract

Two popular variable screening methods under the ultra-high dimensional setting with the desirable sure screening property are the sure independence screening (SIS) and the forward regression (FR). Both are classical variable screening methods and recently have attracted greater attention under the new light of high-dimensional data analysis. We consider a new and simple screening method that incorporates multiple predictors in each step of forward regression, with decision on which variables to incorporate based on the same criterion. If only one step is carried out, it actually reduces to the SIS. Thus it can be regarded as a generalization and unification of the FR and the SIS. More importantly, it preserves the sure screening property and has similar computational complexity as FR in each step, yet it can discover the relevant covariates in fewer steps. Thus, it reduces the computational burden of FR drastically while retaining advantages of the latter over SIS. Furthermore, we show that it can find all the true variables if the number of steps taken is the same as the correct model size, even when using the original FR. An extensive simulation study and application to two real data examples demonstrate excellent performance of the proposed method.

Key words: *Bayesian information criterion; Independence Screening; Model selection / Variable selection; Ultra-high dimensionality.*

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1 Introduction

With rapid advances of modern technology, datasets involving a huge number of variables arise frequently from biological, business, financial, genetics, social studies, etc. Mathematically speaking, we often need to deal with ultra-high dimensional statistical problems by which we mean that $\log(p)$ can be as large as n^a for some constant $a \in (0, 1)$, where p and n denote the dimension and sample size, respectively. For example, in the two genetics examples analyzed in Section 5, p is in tens of thousands whereas n is only around one hundred. Here we focus on multiple linear regression. Extensions to other parametric or semiparametric models are possible but would require additional notation and technical treatments which would obscure the ideas.

In dealing with high-dimensional problems, sparsity is a typical assumption in order to reduce the effective number of parameters and to make estimation feasible. Various penalized regression methods have been proposed for simultaneous selection and estimation under sparsity assumptions. Tibshirani (1996) proposed lasso, whose theoretical properties are investigated by numerous works including Bickel et al. (2009); Knight and Fu (2000); Zhang and Huang (2008); Zhao and Yu (2006). Following its success, many different penalty functions have been proposed to deal with the known issues of lasso, and these methods have been extended to more general regression models. Fan and Li (2001) and Zou (2006) proposed SCAD penalty and adaptive lasso penalty, respectively, which are consistent in variable selection. Zou and Hastie (2005) suggested elastic net by combining lasso and ridge penalties, which can better deal with collinearity in covariates. Fan and Peng (2004), Kim et al. (2008), Huang et al. (2008), Zou and Zhang (2009), and Fan and Lv (2011) investigated theoretical properties of these penalties when the dimension diverges or grows faster than the sample size. Fan and Lv (2013) characterized the asymptotic equivalence of different regularization methods. Fan and Li (2012) studied regularized estimation in linear mixed effects model. In semiparametric additive or varying coefficient models, penalized estimation has been considered by Huang et al. (2010); Lian (2012); Wang et al. (2014); Wei et al. (2011); Xue et al. (2010), among many others. Such methods have become a standard approach to high-dimensional or big data analysis conducted in a diverse spectrum of research fields.

Despite the popularity and success of these penalized methods, they may not perform well due to the “challenges of computational expediency, statistical accuracy and algorithmic stability” (Fan et al.; 2009; Fan and Song; 2010). In particular, computational efficiency is a major concern when the dimension is more than, say, a thousand or even more, because complex optimization algorithms are often used in these methods. To cope with these problems, Fan and Lv (2008) proposed a sure independence screening (SIS) method to screen out unimportant variables

and reduce the dimensionality to a manageable order. Specifically, SIS achieves independence screening by ranking marginal correlations between individual covariates and the response variable. The surprising theoretical result is that this simple procedure possesses the sure screening property, that is, all the predictors in the true model with nonzero coefficients will be included in the estimated model, under mild assumptions. Motivated by its favorable performance and its ease of use in practice, many have followed the lead of Fan and Lv (2008) and proposed various ways to improve its performance and to extend it to different models. Fan and Song (2010) generalized SIS to generalized linear models. Zhu et al. (2011) and Li, Zhong and Zhu (2012) proposed model-free screening without parametric assumption based on sufficient dimension reduction and distance correlation, respectively. Li, Peng, Zhang and Zhu (2012) proposed a robust screening procedure based on Kendall τ 's rank correlation. Cheng et al. (2014); Fan et al. (2011, 2014); Liu et al. (2014); Song et al. (2014) considered independence screening for semiparametric additive and varying-coefficient models. He et al. (2013) studied variable screening in quantile regression for both parametric and semiparametric models. Fan et al. (2015) introduced interaction screening for nonlinear classification.

Soon after the proposal of SIS, Wang (2009) showed that another popular and classical variable selection method, namely the forward regression (FR), also possesses the sure screening property in sparse ultra-high dimensional linear models. Although he did not claim in the work that FR is the only good method for variable screening, the numerical simulations demonstrated the superior performance of FR. In particular, while FR and SIS have similar coverage probabilities the former has a much lower false discovery rate than the latter. This may be due to the fact that FR at least partially takes into account the correlations among covariates by performing multiple linear regression using all the currently incorporated variables, while SIS ignores the effects of all the other covariates when computing the marginal correlation. This also shows up in the technical assumptions required in demonstrating their sure screening property. Specifically, FR only requires the coefficients in the true linear model are sufficiently large (see our definition of β_{\min} given in Theorem 1) i.e. the sparsity assumption. By comparison, SIS typically requires the marginal correlations of the relevant covariates with the response are sufficiently high, which is in general not true even if the coefficients in the true linear model are large. On the other hand, due to the necessity to perform multiple linear regression, FR is certainly slower to compute than SIS. Thus, it would be helpful to reduce the number of steps in FR while keeping its superior properties at the same time.

Motivated by the above mentioned observations, we propose an extension of FR, called greedy forward regression (GFR). It incorporates multiple covariates, say J of them, into the estimated

model in each step of the sequential selection. Note that doing this directly by choosing additional J variables that reduce the sum of squares of residuals (SSR) the most would cause extra computational burden, defeating the computational expediency of using variable screening methods. The reason is this approach would require performing and comparing $\binom{p}{J}$ regression models in each step. Instead, the key idea of our proposal is that we still compute the reduction in SSR when adding only one variable each time and only in the last step we will incorporate multiple variables.

In our theoretical study we show the sure screening property of the proposed GFR method. We also show another stronger theoretical property which is new even when $J = 1$ i.e. when the original FR is used. Specifically, we study the number of steps required to find all the true important variables, and we show that all of them will be identified if we fix the number of steps the same as the true model size. Compared to the standard forward regression, the theoretical challenge here is further caused by the fact that in GFR we compute the reduction in SSR by adding one variable while we include multiple variables in each step. Therefore, our theoretical results are non-trivial. Selection of the tuning parameter J is a minor issue and we provide some general suggestions. Our numerical studies demonstrate that the proposed method retains the advantages of FR over SIS (and ISIS, an iterative variant of SIS) while improving on FR in terms of computational speed.

The details of our algorithm are contained in Section 2, and the theoretical results are given in Section 3. In Section 4 we examine the finite sample performance and compare with the traditional FR, SIS and ISIS via an extensive simulation study. Section 5 presents and discusses application of our method to two genetics datasets. Given in Section 6 are conclusions and future studies. Proofs of the theoretical results are deferred to Section 7.

2 Greedy Forward Regression

We consider standard linear regression models. Let $(\mathbf{X}_1, y_1), \dots, (\mathbf{X}_n, y_n)$ be a sample of independent observations obeying the following form:

$$y_i = \mu + \sum_{j=1}^p X_{ij}\beta_j + \epsilon_i,$$

where $\mathbf{X}_i = (X_{i1}, \dots, X_{ip})^T$ is the p -dimensional covariate vector of the i th observation, μ is the intercept, $\boldsymbol{\beta} = (\beta_1, \dots, \beta_p)^T$ are the unknown coefficients and ϵ_i is the mean zero error contained in the i th observation. In the rest of the paper we assume $\mu = 0$ for simplicity of notation. In matrix notation, we write

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon},$$

with $\mathbf{y} = (y_1, \dots, y_n)^T$, $\mathbf{X} = (\mathbf{X}_1, \dots, \mathbf{X}_p)_{n \times p}$ and $\boldsymbol{\epsilon} = (\epsilon_1, \dots, \epsilon_n)^T$. We focus on the ultra-high dimensional regime where $p \gg n$ and assume a sparse true model in which $p_0 := |\{j : \beta_j \neq 0\}|$ is smaller than n . The true model is denoted by $\mathcal{T} = \{j : \beta_j \neq 0\}$ while the full model is written as $\mathcal{F} = \{1, \dots, p\}$. For any submodel $\mathcal{M} \subseteq \mathcal{F}$, let $\mathbf{X}_{\mathcal{M}}$ be the submatrix of \mathbf{X} associated with \mathcal{M} ; it has $|\mathcal{M}|$ columns. Similarly $\boldsymbol{\beta}_{\mathcal{M}}$ denotes the subvector of $\boldsymbol{\beta}$ containing only components in \mathcal{M} .

In SIS, we rank the importance of variables by $|\mathbf{X}_j^T \mathbf{y}|$, $j \in \mathcal{F}$. It only requires going through each of the p predictors once; therefore SIS is computationally expeditious. However, in general $\beta_j \neq 0$ in the true model does not imply $|\mathbf{X}_j^T \mathbf{y}| \neq 0$ in the marginal model. Thus SIS directly assumes $|\mathbf{X}_j^T \mathbf{y}| \neq 0$ when $\beta_j \neq 0$ in order to guarantee its sure screening property. In the FR algorithm, starting with the null model, we incorporate variables into the model one at a time. At each step, every variable that is not already in the current model is tested and the one which reduces the sum of squares of residuals (SSR) the most is added to the model. Since fitting the submodel in each step is necessary, FR is computationally slower than SIS although it has better control on the false discovery rate. One obvious modification of FR is to consider the best set of J variables that reduce SSR the most if added to the current model together. However, this would increase considerably the computational burden in each step because there are $\binom{p-|\mathcal{M}|}{J}$ possible ways to pick up J variables out of the $p - |\mathcal{M}|$ candidates, if \mathcal{M} is the current model. To avoid this computational problem, in each step of our greedy FR algorithm, we still compute the SSR for each variable outside the current model, and pick the J variables that reduce SSR the most marginally. The algorithm is more formally presented below. In the following we use $\mathbf{P}_{\mathcal{M}} = \mathbf{X}_{\mathcal{M}}(\mathbf{X}_{\mathcal{M}}^T \mathbf{X}_{\mathcal{M}})^+ \mathbf{X}_{\mathcal{M}}$ for the projection matrix associated with $\text{span}\{\mathbf{X}_{\mathcal{M}}\}$, the column span of $\mathbf{X}_{\mathcal{M}}$, where $()^+$ denotes the Moore-Penrose pseudo-inverse. Let $\mathbf{Q}_{\mathcal{M}} = \mathbf{I} - \mathbf{P}_{\mathcal{M}}$ be the projection to the subspace orthogonal to $\text{span}\{\mathbf{X}_{\mathcal{M}}\}$.

Greedy forward regression algorithm:

- (i) Choose the tuning parameter $J \geq 1$. Initially we start with the null model $\mathcal{M}^{(0)} = \emptyset$, and set the step number k as $k = 1$.
- (ii) In step k , let $\mathcal{N}^{(k)} = \{j_1, \dots, j_J\}$ be the index set of the predictors such that the values of $\|\mathbf{P}_{\mathcal{M}^{(k-1)} \cup \{j\}} \mathbf{y}\|$, $j \in \mathcal{N}^{(k)}$, are the J largest among all those $j \in \mathcal{F} \setminus \mathcal{M}^{(k-1)}$. Set $\mathcal{M}^{(k)} = \mathcal{M}^{(k-1)} \cup \mathcal{N}^{(k)}$.
- (iii) Repeat (ii) until at least $n - J + 1$ covariates are incorporated (with more than n covariates the least squares problem becomes unidentified).

Obviously $\|\mathbf{P}_{\mathcal{M}^{(k-1)} \cup \{j\}} \mathbf{y}\|^2 = \|\mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k-1)} \cup \{j\}} \mathbf{y}\|^2$ and the procedure in (ii) is the same as

choosing the predictors associated with the J smallest values of $\|\mathbf{Q}_{\mathcal{M}^{(k-1)} \cup \{j\}} \mathbf{y}\|^2$, i.e. the SSR for model $\mathcal{M}^{(k-1)} \cup \{j\}$, among all $j \in \mathcal{F} \setminus \mathcal{M}^{(k-1)}$.

Similar to forward regression, even with $J > 1$, in each step we perform at most p projections $\mathbf{P}_{\mathcal{M}^{(k-1)} \cup \{j\}} \mathbf{y}$ (or $\mathbf{Q}_{\mathcal{M}^{(k-1)} \cup \{j\}} \mathbf{y}$), $j \in \mathcal{F} \setminus \mathcal{M}^{(k-1)}$. However, we need to keep track of the J largest values along the way, which would incur some extra computational burden. Empirically, we find that such additional book-keeping only adds a small amount of computational time to the algorithm. Detailed computational time comparisons are made in our simulation studies.

Finally, we note that if we set J to be large, say $J = n$ or $n/\log n$ and perform the procedure in (ii) only once, then our algorithm reduces to the marginal independence screening of Fan and Lv (2008). Thus GFR can be regarded as an extension of both FR and independence screening, as taking $J = 1$ it corresponds to FR and choosing J close to n it reduces to SIS. On the other hand, empirically we suggest to choose relatively small value of J such as 2 or 4. Thus GFR builds a bridge between FR and SIS. In the numerical studies we examine its finite sample performance and find that in general it is superior to both FR and SIS.

3 Theoretical Properties

Since more than one predictor is added to the model in each step of the greedy FR algorithm, certainly it will take fewer steps to reach a model with a target model size. For example, as in (iii) of the algorithm we stop as soon as at least $n - J + 1$ predictors are incorporated. However, we are more interested in how this approach affects the consistency of the screening algorithm. Suppose the algorithm builds a finite sequence of models $\mathcal{M}^{(1)}, \dots, \mathcal{M}^{(K)}$, usually referred to as the solution path. We say the algorithm produces a consistent solution path in variable screening if

$$P(\mathcal{T} \subseteq \mathcal{M}^{(k)} \text{ for some } k) \rightarrow 1.$$

This definition was used by Wang (2009) for the original forward regression.

For greedy FR with $J > 1$, the first question is of course whether it still has the desirable screening consistency property. A more refined question is regarding the smallest value of k such that $\mathcal{T} \subseteq \mathcal{M}^{(k)}$. That is, how many iterations are needed before all the relevant predictors are included in the model? Comparing greedy FR with the original FR, intuitively, the worst case that can happen is the additional $J - 1$ covariates selected in each step are not relevant at all and the number of iterations required is the same as that required by FR. The best case, on the other hand, is that all the additional $J - 1$ covariates included in each step are “as relevant as” the top one and the number of iterations is thus reduced by a factor of J . Our first result, given in Theorem 1,

shows that the best case happens at least in the upper bound we obtain for the number of iterations required by the greedy FR. Thus, it has the potential to incorporate all the relevant predictors in fewer steps than FR does. Our second theoretical result given in Theorem 2 tries to answer the same question, but from a slightly different perspective. We consider the following question: under what conditions will the greedy FR with $J \geq 1$ incorporate at least one relevant predictor in each step? When this happens, it will incorporate all relevant predictors after at most p_0 steps. It turns out this happens under reasonable assumptions. This result appears to be new even for the case of $J = 1$, i.e. the FR, to our knowledge.

We first define restricted eigenvalues and restricted correlations, which have been used for example in Bickel et al. (2009). For an integer s , the restricted eigenvalues are defined as

$$\phi(s) = \min_{\|\mathbf{x}\|_0 \leq s} \frac{\mathbf{x}^T \mathbf{X}^T \mathbf{X} \mathbf{x}}{n \|\mathbf{x}\|^2} \quad \text{and} \quad \Phi(s) = \max_{\|\mathbf{x}\|_0 \leq s} \frac{\mathbf{x}^T \mathbf{X}^T \mathbf{X} \mathbf{x}}{n \|\mathbf{x}\|^2},$$

and the restricted correlations are

$$\theta_{s_1, s_2} = \max \left\{ \frac{\mathbf{x}_1^T \mathbf{X}_{\mathcal{M}_1}^T \mathbf{X}_{\mathcal{M}_2} \mathbf{x}_2}{n \|\mathbf{x}_1\| \|\mathbf{x}_2\|} : \mathcal{M}_1 \cap \mathcal{M}_2 = \emptyset, |\mathcal{M}_1| \leq s_1, |\mathcal{M}_2| \leq s_2 \right\}.$$

In particular, by definition, we have $\|\mathbf{X}_j\|^2 \leq n\Phi(1)$, where \mathbf{X}_j is the j -th column of \mathbf{X} . In some literature, it is assumed that $\phi(s)$ and $\Phi(s)$ are bounded and bounded away from zero for $s = O(n^\alpha)$ with some value $\alpha < 1$, which will simplify the bounds below. We choose to explicitly track these quantities for the sake of generality, and only require they are nonzero.

Theorem 1 *Assume ϵ_i has a subgaussian distribution. That is, there exists a constant $c > 0$ such that $E[\exp\{t\epsilon_i\}] \leq \exp\{ct^2\}$. Let $\beta_{\min} = \min_{j \in \mathcal{T}} |\beta_j|$. Suppose K_0 is an integer satisfying*

$$K_0 > \frac{2\|\mathbf{y}\|^2 \Phi(J) \Phi(1)}{n \phi^3(p_0 K_0 J) J \beta_{\min}^2} \quad (1)$$

and

$$p_0 K_0 J \log(p) = o_p\left(\frac{n \phi^2(p_0 K_0 J) \beta_{\min}^2}{\Phi(1)}\right),$$

then

$$P(\mathcal{T} \subseteq \mathcal{M}^{(p_0 K_0)}) \rightarrow 1.$$

That is, all relevant variables are incorporated after $p_0 K_0$ steps.

Remark 1 *Suppose that for a constant C sufficiently large, $\tau_1 < \phi(s) \leq \Phi(s) \leq \tau_2$ for two positive constants when $s \leq Cp_0/\beta_{\min}^2$. If we further assume reasonably that $\|\mathbf{y}\|^2 = O_p(n)$, then*

K_0 can be chosen to be $K_0 = O_p(1/(J\beta_{\min}^2))$ and at most $O_p(p_0/(J\beta_{\min}^2))$ steps are required. When $J = 1$, this gives a $O_p(p_0/\beta_{\min}^2)$ bound on the number steps required, which is better than the $O_p(p_0^2/\beta_{\min}^4)$ bound stated in Theorem 1 of Wang (2009). The reason for the improvement here is that we use a slightly tighter lower bound in (7) of the proof, compared to their equation (B.6).

Remark 2 Some assumptions are implicit in the statement of the theorem above. These include $\phi(p_0 K_0 J) \neq 0$ and $\beta_{\min} \neq 0$. Also implicitly assumed is $p_0 K_0 \leq \lfloor n/J \rfloor$, where $\lfloor n/J \rfloor$ denotes the integer part of n/J , since we will terminate the algorithm after $\lfloor n/J \rfloor$ iterations.

Remark 3 From the proof it can be seen that the constant 2 in (1) can be replaced by any fixed constant larger than 1.

From Theorem 1, it is seen that using $J > 1$ the greedy FR algorithm will discover all the relevant predictors in fewer steps. However, the trade-off is that each step of greedy FR incorporates J covariates which makes the computation slower when comparing the k -th step of greedy FR with that of the original FR. Although the theorem seems to suggest that a larger value of J is better, we note that it merely provides an upper bound on the number of iterations required. Another hidden condition is that, since $p_0 K_0 J \approx n$ and $K_0 \geq 1$, we need $J \leq n/p_0$. Empirically, we find a relatively small value of J , say $J = 2$ or 4, works better.

Theorem 2 Assume the noises are subgaussian. Suppose for some $\eta > 0$,

$$\frac{\phi^3(p_0 J) J}{\Phi(1) p_0} \geq (1 + \eta) \left(\theta_{J, p_0} + \frac{\theta_{J, (p_0-1)J} \theta_{(p_0-1)J, p_0}}{\phi(p_0 J)} \right)^2, \quad (2)$$

and

$$p_0 J \log p = o_p \left(\frac{n}{J \Phi(1)} \left(\theta_{J, p_0} + \frac{\theta_{J, (p_0-1)J} \theta_{(p_0-1)J, p_0}}{\phi(p_0 J)} \right)^2 \beta_{\min}^2 \right).$$

Then each step of the greedy FR will incorporate at least one relevant predictor and thus all the relevant predictors will be included in at most p_0 steps.

Remark 4 The expressions of our assumptions can be simplified under restricted isometry constant δ_s which is defined as the smallest quantity such that

$$\left\{ \frac{\mathbf{x}^T \mathbf{X}^T \mathbf{X} \mathbf{x}}{n \|\mathbf{x}\|^2} : \|\mathbf{x}\|_0 \leq s, \mathbf{x} \neq \mathbf{0} \right\} \subseteq [1 - \delta_s, 1 + \delta_s].$$

For example, following from the fact that $\theta_{s_1, s_2} \leq \delta_{s_1 + s_2}$ (Lemma 1.1 of Candes and Tao (2005)), condition (2) is implied by

$$\frac{(\delta_{p_0+J}(1 + \delta_{p_0 J}) + \delta_{p_0 J}^2)^2}{(1 - \delta_{p_0 J})^5} \leq \frac{J}{p_0(1 + \eta)(1 + \delta_1)}. \quad (3)$$

Remark 5 *Intuitively, since each step of the greedy FR includes more additional covariates, the probability that a relevant covariate is incorporated is higher than using the original FR. Mathematically, it is unclear whether (2) or (3) represent a less stringent assumption for larger values of J , as both sides of the equation are generally increasing with J .*

In practice, one needs to select a model along the solution path. As in Wang et al. (2007) and Chen and Chen (2008), we use the BIC-type criterion defined as

$$BIC(k) = n \log(\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2) + (kJ) \log n.$$

Then we choose the final model as the one which minimizes $BIC(k)$ among $k = 0, 1, \dots, [n/J]$. The following theorem shows the screening consistency property when we use the BIC stopping criterion in the greedy forward regression.

Theorem 3 *Under the same conditions as in Theorem 1, and the assumptions that*

$$J = o(n/\log n) \quad \text{and} \quad J = o\left(\frac{\phi^3(p_0 K_0 J) n^2 \beta_{\min}^2}{2\Phi(J)\Phi(1)\|\mathbf{y}\|^2 \log n}\right),$$

we have

$$P(\mathcal{T} \subseteq \mathcal{M}^{(\hat{k})}) \rightarrow 1,$$

where $\hat{k} = \arg \min_{0 \leq k \leq [n/J]} BIC(k)$.

4 Simulation Results

In this section, we perform Monte Carlo simulations to evaluate finite sample performance of the proposed greedy forward regression (GFR) algorithm for ultra-high dimensional variable screening. We consider the following three simulation examples.

Example 1 In this example, the components of $\mathbf{X} = (X_1, \dots, X_p)^T$ are generated from a multivariate normal distribution $N(0, \Sigma)$, and Σ is a block diagonal covariance matrix with 2×2 blocks $\begin{pmatrix} 1 & -0.4 \\ -0.4 & 1 \end{pmatrix}$. The size of the true model is chosen to be $p_0 = 8$ with $\boldsymbol{\beta} = (2, 3, 2, 3, 2, 3, 2, 3, 0, \dots, 0)^T$.

Example 2 (Autoregressive correlation). For this simulation example, \mathbf{X} is a p -dimensional multivariate normal random vector with mean zero and covariance matrix (σ_{ij}) with $\sigma_{ij} = 0.5^{|i-j|}$ for $1 \leq i, j \leq p$. The 1st, 4th and 7th components of $\boldsymbol{\beta}$ are 3, 1.5 and 2, respectively, and the other elements of $\boldsymbol{\beta}$ are fixed to be zero.

Example 3. Consider Example III in Section 4.2.3 of Fan and Lv (2008) with

$$Y = 5X_1 + 5X_2 + 5X_3 - 15\sqrt{0.5}X_4 + X_5 + \epsilon, \quad (4)$$

where $(X_1, X_2, X_3, X_6, \dots, X_p)^T$ are generated from a multivariate normal distribution $N(0, \Sigma)$ with entries of $\Sigma = (\sigma_{ij})_{(p-2) \times (p-2)}$ being $\sigma_{ii} = 1, i = 1, \dots, p-2$ and $\sigma_{ij} = 0.6, i \neq j$, and $X_4 \sim N(0, 1)$ has correlation coefficient $\sqrt{0.5}$ with all the other $p-1$ variables whereas $X_5 \sim N(0, 1)$ is uncorrelated with all the other $p-1$ variables. In this example the true variable X_5 has an even weaker marginal correlation with y than the irrelevant variables X_6, \dots, X_p do.

In all the above three examples, the noise ϵ is generated from a normal distribution with mean 0 and variance σ^2 , and the variance σ^2 is selected so that the $R^2 = \text{Var}\{\mathbf{X}^T \boldsymbol{\beta}\} / \text{Var}(y)$ is approximately 50%, 70% or 90%. We considered sample size $n = 150$ and three different predictor dimensions ($p = 500, 1000$ or 2000). For each case, we repeated the experiment 200 times. For GFR, we used $J = 1, 2$ or 4 . Obviously the GFR method reduces to the FR method proposed by Wang (2009) when $J = 1$.

Let $\hat{\boldsymbol{\beta}}_{(k)} = (\hat{\beta}_{1(k)}, \dots, \hat{\beta}_{p(k)})^T \in \mathbb{R}^p$ denote the estimator obtained in the k th simulation replication (using some stopping criterion). The selected model is taken as $\widehat{\mathcal{M}}_{(k)} = \{j : |\hat{\beta}_{j(k)}| > 0, j = 1, \dots, p\}$. We use the following performance measures to evaluate the methods: (1) The average number of false positives (AFP); (2) The average number of false negatives (AFN); (3) The average model size (AMS) $200^{-1} \sum_k |\widehat{\mathcal{M}}_{(k)}|$; (4) The coverage probability (CP) $200^{-1} \sum_k I(\mathcal{T} \subseteq \widehat{\mathcal{M}}_{(k)})$.

The simulation study was carried out using MATLAB on a desktop computer with 3.20GHz CPU and 4GB RAM and the results under three scenarios are reported in Tables 1–9.

Scenario (i) We ran the GFR procedure exactly p_0 iterations, where p_0 is the true number of nonzero coefficients of $\boldsymbol{\beta}$ in the true model, and compute the average computational time when running stops (Time, in seconds) and CP. This is mainly to illustrate our Theorem 2 to see whether all the true nonzero coefficients can be identified in exactly p_0 steps. The results are reported in Tables 1, 4 and 7, for the three examples, respectively. We can see from these tables that when increasing from $J = 1$ to either $J = 2$ or $J = 4$, most of the time there is a significant increase in CP while only small additional cost in computational time is needed.

Scenario (ii) We ran the GFR till the end (incorporating close to n variables in the model) and also recorded the time point when all relevant variables are incorporated into the estimated model (this time point is taken to be the time when running stops if not all relevant variables are incorporated when running stops). We computed the average computational time when running stops (time1), the average computational time when all nonzero coefficient are identified (time2), the average number of iterations (iter) and the average model size (AMS) when all nonzero coefficients

are identified, and CP when running stops. The results are reported in Tables 2, 5 and 8. Compared to the case $J = 1$, the CP values when running stops are often, although only slightly, larger when $J = 2$ or 4. Note this is achieved with much shorter computational time (time1 reported in these tables). Also, the time to the point when all the relevant covariates are incorporated is in general shorter for larger values of J .

Scenario (iii) Finally, we computed CP, AFP, AFN, AMS for the model selected by BIC, and the average computational time when running till BIC achieves its minimum value (time3). Note the AMS reported here is for the model selected based on BIC while in scenario (ii) the AMS is based on the model when all relevant covariates are incorporated. We also included SIS and ISIS for comparison. Following Fan and Lv (2008) and Wang (2009), the size of the SIS model was fixed to be $\lfloor n/\log n \rfloor$, and for the ISIS method, a total of $\lfloor \log n - 1 \rfloor$ ISIS steps were conducted and $\lfloor n/\log n \rfloor$ variables were selected in each step. The results are reported in Tables 3, 6 and 9. The computational time (Time3) of GFR decreases as J increases. In terms of the criteria CP, AFP, AFN and AMS, the performances of GFR using different values of J are similar. One exception is example 3 (Table 9) where the CP for $J = 4$ is low compared to $J = 1, 2$ when the signal is strong ($R^2 = 90\%$). However, by Scenario (ii), when running stops the CP for $J = 4$ is satisfactory. This suggests that the problem resides in the fact that the BIC criterion stops the procedure too early. Finding a better criterion than BIC is thus an important problem, but very challenging one at the same time, which is outside the scope of the current paper. In Examples 1 and 3, SIS often has lower CP than GFR and FR do, but has higher CP in Example 2. However, note that the AMS (and AFP) of SIS is much larger than that of GFR. CP for ISIS is large for Examples 1 and 2, which is however achieved with even larger AMS and AFP.

5 Applications to Real Datasets

We applied GFR to two real data examples and compare it with FR, SIS and ISIS. First we considered the breast cancer dataset reported by van't Veer et al. (2002), which consists of expression levels for 24481 gene probes and seven clinical risk factors (age, tumor size, histological grade, angioinvasion, lymphocytic infiltration, estrogen receptor, and progesterone receptor status) for 97 lymph node-negative breast cancer patients 55 years old or younger. Among the 97 patients, 46 developed distant metastases within 5 years and the other 51 remained metastases free for more than 5 years. Yu et al. (2012) proposed a ROC based approach to rank importance of the genes in predicting distant metastases after adjusting for the clinical risk factors. In their analysis, genes with severe missingness were removed, and the other 24188 genes remained. The gene expression

data were normalized such that all the variables have sample mean 0 and standard deviation 1.

Using their ranking methods Yu et al. (2012) found that, among the 24188 genes, gene 271 is the top one related to distant metastases within 5 years. Thus it is interesting to find genes that are related to gene 271. Genes identified by FR, and the proposed GFR method with $J = 2$ or 4 are listed in Table 10. In addition, SIS found 21 genes which include all the genes identified by the GFR methods except gene 5342, and ISIS found 63 genes which include all the genes identified by GFR methods. Then we compare the prediction mean squared errors (PMSE) of these different methods. For this purpose we randomly selected 90 observations as the training set and used the rest 7 observations for testing purpose. This procedure was repeated 20 times. The average of PMSEs over the 20 repetitions are reported in Table 11. From the table we observe that GFR with $J = 4$ has the smallest prediction error. Furthermore, note that ISIS has larger PMSE than SIS does, possibly because it includes more unimportant variables in the model.

Next we applied the proposed screening methods to a dataset arising from a microarray study in which expression quantitative trait locus (eQTL) mapping in laboratory rats was used to investigate gene regulation in the mammalian eye and to identify genetic variation relevant to human eye disease (Scheetz et al.; 2006). This dataset contains expressions of 31042 probe sets on 120 rats. Our goal is to find probes that are related to that of gene TRIM32, which has been found to cause Bardet-Biedl syndrome. The probe from TRIM32, 1389163_at, is thus used as the response variable. Similar to Huang et al. (2008), 3000 probes with the largest variances in expression values were used as covariates in our analysis.

Probes found by FR, and the GFR method with $J = 2$ or 4 are listed in Table 12. SIS found 25 probes which include all those identified by the GFR methods except 1392692_at and 1378099_at, and ISIS found 75 probes which include all those identified by GFR methods except 1378099_at. To compare the prediction mean squared errors of these different methods, we randomly split the data into a training set of size 80 and a testing set of size 40. This procedure was repeated 1000 times. The average PMSEs of the different methods over the 1000 repetitions are reported in Table 13. Again, we can see that GFR with $J = 4$ has the smallest prediction error whereas the prediction error of ISIS is significantly larger than that of the other methods.

6 Conclusions and Future Studies

We propose GFR, a modification of the FR for sure screening of variables in sparse ultra-high dimensional linear regression, and show its theoretical and numerical advantages over the original FR. The main message is that GFR is faster to compute and its performance is comparable in terms

of CP, AFP and AFN. Besides, when the signal is weaker (R^2 is lower), the simulation results suggest that the GFR tends to pick up more true variables than the FR does (yielding smaller AFN) at the expense of slightly larger AFP only. In addition, GFR appears to cope with correlation between the covariates better than FR does. The theoretical insights into these phenomena deserve future study. As mentioned in Section 4, it remains an important and challenging problem to construct alternative stopping criteria in order to improve the performance in terms of CP and AFN. FR is known to be in general better than SIS or ISIS in yield a parsimonious model. The real data examples presented in Section 5 indicate that the GFR preserves this property, and even improves on FR in terms of prediction error. The GFR approach may be extended to other parametric models, such as generalized linear regression, and even to semiparametric models such as varying coefficient and semivarying coefficient models. Such extensions are non-trivial, however, and require further study.

7 Technical proofs

Proof of Theorem 1. We start by assuming that no relevant predictors are contained in $\mathcal{N}^{(k+1)}$. Let $\mathbf{X}_{(k+1)} = \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{N}^{(k+1)}} = \mathbf{X}_{\mathcal{N}^{(k+1)}} - \mathbf{X}_{\mathcal{M}^{(k)}} (\mathbf{X}_{\mathcal{M}^{(k)}}^T \mathbf{X}_{\mathcal{M}^{(k)}})^{-1} \mathbf{X}_{\mathcal{M}^{(k)}}^T \mathbf{X}_{\mathcal{N}^{(k+1)}}$ be the projection of $\mathbf{X}_{\mathcal{N}^{(k+1)}}$ onto the space orthogonal to $\text{span}\{\mathcal{M}^{(k)}\}$. We have

$$\begin{aligned} \mathbf{P}_{\mathcal{M}^{(k+1)}} &= \mathbf{P}_{\mathcal{M}^{(k)} \cup \mathcal{N}^{(k+1)}} \\ &= \mathbf{P}_{\mathcal{M}^{(k)}} + \mathbf{X}_{(k+1)} (\mathbf{X}_{(k+1)}^T \mathbf{X}_{(k+1)})^{-1} \mathbf{X}_{(k+1)}^T \\ &= \mathbf{P}_{\mathcal{M}^{(k)}} + \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{N}^{(k+1)}} (\mathbf{X}_{\mathcal{N}^{(k+1)}}^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{N}^{(k+1)}})^{-1} \mathbf{X}_{\mathcal{N}^{(k+1)}}^T \mathbf{Q}_{\mathcal{M}^{(k)}}, \end{aligned} \quad (5)$$

where in the second equality above we used that columns of $\mathbf{X}_{\mathcal{M}^{(k)}}$ and columns of $\mathbf{X}_{(k+1)}$ are orthogonal. Using (5), the change of SSR in the k -th step is

$$\begin{aligned} \|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2 &= \mathbf{y}^T (\mathbf{Q}_{\mathcal{M}^{(k)}} - \mathbf{Q}_{\mathcal{M}^{(k+1)}}) \mathbf{y} \\ &= \mathbf{y}^T (\mathbf{P}_{\mathcal{M}^{(k+1)}} - \mathbf{P}_{\mathcal{M}^{(k)}}) \mathbf{y} \\ &= \|(\mathbf{X}_{\mathcal{N}^{(k+1)}}^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{N}^{(k+1)}})^{-1/2} \mathbf{X}_{\mathcal{N}^{(k+1)}}^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 \\ &\geq \frac{1}{n\Phi(J)} \|\mathbf{X}_{\mathcal{N}^{(k+1)}}^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 \\ &= \frac{1}{n\Phi(J)} \sum_{j \in \mathcal{N}^{(k+1)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2. \end{aligned}$$

For $j \in \mathcal{N}^{(k+1)}$, we have

$$|\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \geq n\phi(kJ + 1) |(\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j)^{-1/2} \mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2$$

$$\begin{aligned}
&\geq n\phi(kJ+1) \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |(\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j)^{-1/2} \mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \\
&\geq \frac{\phi(kJ+1)}{\Phi(1)} \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2,
\end{aligned}$$

where in the first inequality we used Lemma 1 and in the second inequality we used that $\mathcal{N}^{(k+1)}$ contains the indices with the J largest values of

$$\|\mathbf{P}_{\mathcal{M}^{(k)} \cup \{j\}} \mathbf{y}\|^2 = \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + |(\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j)^{-1/2} \mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2$$

(the above equality follows from the same arguments as for (5)) among all $j \in \mathcal{F} \setminus \mathcal{M}^{(k)}$ and that no relevant covariate is contained in $\mathcal{N}^{(k+1)}$. Thus we have

$$\begin{aligned}
&\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2 \\
&\geq \frac{\phi(kJ+1)}{n\Phi(J)\Phi(1)} \cdot J \cdot \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \\
&\geq \frac{\phi(kJ+1)}{n\Phi(J)\Phi(1)} \cdot J \cdot \left(\max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}| - \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \boldsymbol{\epsilon}| \right)^2 \quad (6)
\end{aligned}$$

where the last inequality follows from $\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{M}^{(k)}} = \mathbf{0}$. Furthermore, let t_k be the number of truly relevant covariates in $\mathcal{M}^{(k)}$, we have

$$\begin{aligned}
&\max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}|^2 \\
&\geq \frac{1}{p_0 - t_k} \|\mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|^2 \\
&\geq \frac{n^2 \phi^2(p_0 - t_k + kJ)}{p_0 - t_k} \|\boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|^2 \\
&\geq n^2 \phi^2(p_0 - t_k + kJ) \beta_{\min}^2, \quad (7)
\end{aligned}$$

using Lemma 1.

Under the subgaussian assumption of the noise, and noticing that $\|\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}}\|^2 \leq \|\mathbf{X}_j\|^2 \leq n\Phi(1)$, we have

$$P(|\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \boldsymbol{\epsilon}| > t) \leq c_1 \exp\{-c_2 t^2 / (n\Phi(1))\},$$

and by the union bound

$$P\left(\sup_{j \in \mathcal{F}, |\mathcal{M}| \leq M} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}} \boldsymbol{\epsilon}| > t\right) = O(\exp\{-c_2 t^2 / (n\Phi(1)) - M \log p\}). \quad (8)$$

If (as we have assumed)

$$p_0 K_0 J \log(p) = o_p\left(\frac{n\phi^2(p_0 K_0 J)\beta_{\min}^2}{\Phi(1)}\right), \quad (9)$$

the second term in (6) is dominated by the first term in (6). Then for $k = 1, \dots, p_0 K_0$, we have by (9) above and (6)-(8) that

$$\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2 \geq \frac{\phi(p_0 K_0 J) J n^2 \phi^2(p_0 K_0 J) \beta_{\min}^2}{n\Phi(J)\Phi(1)} \frac{1}{2},$$

if step k does not incorporate any relevant covariate.

Since K_0 is such that

$$K_0 > \frac{\|\mathbf{y}\|^2}{\frac{\phi(p_0 K_0 J) J n^2 \phi^2(p_0 K_0 J) \beta_{\min}^2}{n\Phi(J)\Phi(1)}},$$

we see that within every K_0 steps there is at least one relevant covariate included. Thus after at most $p_0 K_0$ steps all the relevant covariates are included (with the total number of covariates included at most $p_0 K_0 J$). \square

Lemma 1 For two models $\mathcal{M}_1, \mathcal{M}_2$, with $\mathcal{M}_1 \cap \mathcal{M}_2 = \emptyset$ and $|\mathcal{M}_1 \cup \mathcal{M}_2| = s$, we have $\inf_{\|\mathbf{u}\|=1} \mathbf{u}^T \mathbf{X}_{\mathcal{M}_1}^T \mathbf{Q}_{\mathcal{M}_2} \mathbf{X}_{\mathcal{M}_1} \mathbf{u} \geq n\phi(s)$.

Proof. We write

$$\mathbf{Q}_{\mathcal{M}_2} \mathbf{X}_{\mathcal{M}_1} = \mathbf{X}_{\mathcal{M}_1} - \mathbf{X}_{\mathcal{M}_2} (\mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_2})^{-1} \mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_1} = (\mathbf{X}_{\mathcal{M}_1}, \mathbf{X}_{\mathcal{M}_2}) \begin{pmatrix} \mathbf{I} \\ -(\mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_2})^{-1} \mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_1} \end{pmatrix}.$$

Then

$$\begin{aligned} & \mathbf{u}^T \mathbf{X}_{\mathcal{M}_1}^T \mathbf{Q}_{\mathcal{M}_2} \mathbf{X}_{\mathcal{M}_1} \mathbf{u} \\ &= \mathbf{u}^T [\mathbf{I}, -\mathbf{X}_{\mathcal{M}_1}^T \mathbf{X}_{\mathcal{M}_2} (\mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_2})^{-1}] (\mathbf{X}_{\mathcal{M}_1 \cup \mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_1 \cup \mathcal{M}_2}) [\mathbf{I}, -\mathbf{X}_{\mathcal{M}_1}^T \mathbf{X}_{\mathcal{M}_2} (\mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_2})^{-1}]^T \mathbf{u}. \end{aligned}$$

Since $\|\mathbf{u}^T [\mathbf{I}, -\mathbf{X}_{\mathcal{M}_1}^T \mathbf{X}_{\mathcal{M}_2} (\mathbf{X}_{\mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_2})^{-1}]\| \geq \|\mathbf{u}\| = 1$, and the smallest eigenvalue of $\mathbf{X}_{\mathcal{M}_1 \cup \mathcal{M}_2}^T \mathbf{X}_{\mathcal{M}_1 \cup \mathcal{M}_2}$ is bounded below by $n\phi(s)$, thus we see the claim is true. \square

Proof of Theorem 2. Suppose each of the first k steps identifies at least one relevant covariate. Assume t_k , the number of relevant covariates in $\mathcal{M}^{(k)}$, is still less than p_0 . Consider step $k+1$ of the algorithm. Let $R_j^{(k)} = \|\mathbf{P}_{\mathcal{M}^{(k)} \cup \{j\}} \mathbf{y}\|^2$. To show that the k -th step also identifies at least one relevant covariate, we only need to show that $\max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} R_j^{(k)}$ is larger than the J -th largest value of $\{R_j^{(k)} : j \in \mathcal{T} \setminus \mathcal{M}^{(k)}\}$.

Similar to (5), we have

$$\mathbf{P}_{\mathcal{M}^{(k)} \cup \{j\}} = \mathbf{P}_{\mathcal{M}^{(k)}} + \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j (\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j)^{-1} \mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}}, \quad (10)$$

which gives

$$\begin{aligned} R_j^{(k)} &= \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \left\| \frac{\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j \mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}}}{\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j\|^2} \mathbf{y} \right\|^2 \\ &= \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \frac{|\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2}{\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j\|^2}. \end{aligned}$$

Thus

$$\begin{aligned} &\max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} R_j^{(k)} \\ &\geq \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \frac{1}{n\Phi(1)} \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \\ &\geq \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \frac{1}{n\Phi(1)} \left(\max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}| - \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \boldsymbol{\epsilon}| \right)^2, \end{aligned}$$

Using (7), we have

$$\max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}| \geq \frac{n\phi(p_0 - t_k + kJ)}{\sqrt{p_0 - t_k}} \|\boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|.$$

On the other hand, letting \mathcal{J} be the set of indices of the J largest values of $\{R_j^{(k)} : j \in \mathcal{T}^c \setminus \mathcal{M}^{(k)}\}$, then the J -th largest value of $\{R_j^{(k)} : j \in \mathcal{T}^c \setminus \mathcal{M}^{(k)}\}$ is bounded above by

$$\begin{aligned} &\|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \frac{1}{J} \sum_{j \in \mathcal{J}} \frac{|\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2}{\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_j\|^2} \\ &\leq \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \frac{1}{nJ\phi(kJ+1)} \sum_{j \in \mathcal{J}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \\ &\leq \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 + \frac{1+\eta}{nJ\phi(kJ+1)} \sum_{j \in \mathcal{J}} \left(|\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}|^2 + \frac{1}{\eta} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \boldsymbol{\epsilon}|^2 \right), \end{aligned}$$

for any $\eta > 0$. Furthermore,

$$\begin{aligned} &\sum_{j \in \mathcal{J}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}|^2 \\ &= \|\mathbf{X}_{\mathcal{J}}^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|^2 \\ &\leq (\|\mathbf{X}_{\mathcal{J}}^T \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\| + \|\mathbf{X}_{\mathcal{J}}^T \mathbf{X}_{\mathcal{M}^{(k)}} (\mathbf{X}_{\mathcal{M}^{(k)}}^T \mathbf{X}_{\mathcal{M}^{(k)}})^{-1} \mathbf{X}_{\mathcal{M}^{(k)}}^T \mathbf{X}_{\mathcal{T} \setminus \mathcal{M}^{(k)}} \boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|)^2 \\ &\leq (n\theta_{J,p_0-t_k} \|\boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\| + \frac{n\theta_{J,kJ}\theta_{kJ,p_0-t_k}}{\phi(kJ)} \|\boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|)^2 \end{aligned}$$

Thus, we have that the J -th largest value of $\{R_j^{(k)} : j \in \mathcal{T}^c \setminus \mathcal{M}^{(k)}\}$ is bounded above by

$$\begin{aligned} \|\mathbf{P}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 &+ \frac{1+\eta}{nJ\phi(kJ+1)} \left(n\theta_{J,p_0-t_k} + \frac{n\theta_{J,kJ}\theta_{kJ,p_0-t_k}}{\phi(kJ)} \right)^2 \|\boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|^2 \\ &+ \frac{1+\eta}{n\eta\phi(kJ+1)} \max_{j \in \mathcal{T}^c \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \boldsymbol{\epsilon}|^2. \end{aligned}$$

Thus if

$$\frac{n^2\phi^2(p_0 - t_k + kJ)}{n\Phi(1)(p_0 - t_k)} \geq \frac{1+\eta}{nJ\phi(kJ+1)} \left(n\theta_{J,p_0-t_k} + \frac{n\theta_{J,kJ}\theta_{kJ,p_0-t_k}}{\phi(kJ)} \right)^2, \quad (11)$$

for some constant $\eta > 0$, and

$$\max_{j \in \mathcal{F}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \boldsymbol{\epsilon}|^2 = o_p \left(\frac{1}{J} \left(n\theta_{J,p_0-t_k} + \frac{n\theta_{J,kJ}\theta_{kJ,p_0-t_k}}{\phi(kJ)} \right)^2 \|\boldsymbol{\beta}_{\mathcal{T} \setminus \mathcal{M}^{(k)}}\|^2 \right), \quad (12)$$

then at least one relevant predictor will be selected in step $k+1$. Noting $t_k \geq k$ and $p_0 - t_k + kJ \leq p_0J$, (11) is implied by

$$\frac{\phi^3(p_0J)J}{\Phi(1)p_0} \geq (1+\eta) \left(\theta_{J,p_0} + \frac{\theta_{J,(p_0-1)J}\theta_{(p_0-1)J,p_0}}{\phi(p_0J)} \right)^2.$$

In addition, by (8), (12) is implied by

$$p_0J \log p = o_p \left(\frac{n}{J\Phi(1)} \left(\theta_{J,p_0} + \frac{\theta_{J,(p_0-1)J}\theta_{(p_0-1)J,p_0}}{\phi(p_0J)} \right)^2 \beta_{\min}^2 \right).$$

□

Proof of Theorem 3. By Theorem 1, we know that $\mathcal{T} \subseteq \mathcal{M}^{p_0K_0}$ with probability approaching 1. We only need to show that

$$P \left(\min_{\mathcal{T} \setminus \mathcal{M}^{(k)} \neq \emptyset, k \leq p_0K_0} BIC(k) - BIC(k+1) > 0 \right) \rightarrow 1.$$

We have shown in the proof of Theorem 1 that if $\mathcal{N}^{(k+1)} \cap \mathcal{T} = \emptyset$,

$$\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2 \geq \frac{\phi(p_0K_0J)J}{n\Phi(J)\Phi(1)} \frac{n^2\phi^2(p_0K_0J)\beta_{\min}^2}{2}.$$

On the other hand, if $\mathcal{N}^{(k+1)} \cap \mathcal{T} \neq \emptyset$, using almost the same arguments, we have with probability approaching 1,

$$\begin{aligned} \|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2 &\geq \frac{1}{n\Phi(J)} \sum_{j \in \mathcal{N}^{(k+1)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \\ &\geq \frac{1}{n\Phi(J)} \max_{j \in \mathcal{N}^{(k+1)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \end{aligned}$$

$$\begin{aligned}
&\geq \frac{\phi(kJ+1)}{n\Phi(J)\Phi(1)} \cdot \max_{j \in \mathcal{T} \setminus \mathcal{M}^{(k)}} |\mathbf{X}_j^T \mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}|^2 \\
&\geq \frac{\phi(p_0 K_0 J)}{n\Phi(J)\Phi(1)} \frac{n^2 \phi^2(p_0 K_0 J) \beta_{\min}^2}{2}.
\end{aligned}$$

Note the only difference from the $\mathcal{N}^{(k+1)} \cap \mathcal{T} = \emptyset$ case is the removal of a factor of J in the lower bound. Then

$$\begin{aligned}
BIC(k) - BIC(k+1) &= n \log(\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2) - n \log(\|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2) - J \log(n) \\
&= n \log \left(1 + \frac{\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2}{\|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2} \right) - J \log(n).
\end{aligned}$$

Using the elementary inequality $\log(1+x) \geq \min\{\log 2, x/2\}$, the lower bound for $\|\mathbf{Q}_{\mathcal{M}^{(k)}} \mathbf{y}\|^2 - \|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2$ above, and the fact $\|\mathbf{Q}_{\mathcal{M}^{(k+1)}} \mathbf{y}\|^2 \leq \|\mathbf{y}\|^2$, we get

$$BIC(k) - BIC(k+1) = \min \left\{ n \log 2, \frac{\phi^3(p_0 K_0 J) n^2 \beta_{\min}^2}{2\Phi(J)\Phi(1)\|\mathbf{y}\|^2} \right\} - J \log n.$$

Under our assumptions, the quantity on the RHS of the above equality is positive with probability approaching 1. Hence the proof is completed. \square

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Table 1: Simulation results of Example 1, scenario (i).

p	R^2	FR		GFR($J = 2$)		GFR($J = 4$)	
		CP	Time (s)	CP	Time (s)	CP	Time (s)
500	90%	0.9950	1.1399	1	1.4808	1	1.8915
1000		0.9850	2.3243	1	3.0221	1	3.8769
2000		0.9950	4.7588	1	6.1619	1	7.9348
500	70%	0.9100	1.1315	0.9850	1.4753	0.9950	1.8946
1000		0.8250	2.3116	0.9700	3.0089	0.9500	3.8820
2000		0.6850	4.7530	0.9250	6.1739	0.9300	7.9421
500	50%	0.1350	1.1316	0.4350	1.4797	0.4600	1.8943
1000		0.0600	2.3079	0.1600	3.0153	0.2350	3.8792
2000		0.0150	4.7561	0.0250	6.1693	0.0350	7.9297

Table 2: Simulation results of Example 1, scenario (ii).

Method	p	R^2	CP	AMS	iter	Time1 (s)	Time2 (s)
FR	500		1	8.0100	8.0100	32.9721	1.1024
	1000	90%	1	8.0200	8.0200	68.9648	2.2070
	2000		1	8.0100	8.0100	141.7676	4.4289
	500		0.9950	8.3878	8.3878	32.8481	1.8205
	1000	70%	1	8.2400	8.2400	69.1548	2.3230
	2000		0.9500	8.3469	8.3469	141.4304	7.4696
	500		0.5250	16.8889	16.8889	33.0695	17.3780
	1000	50%	0.2100	16.6000	16.6000	69.5911	57.0291
	2000		0.0600	24.6667	24.6667	142.5579	135.4758
GFR($J = 2$)	500		1	8.0600	4.0300	17.0107	0.4833
	1000	90%	1	8.1000	4.0500	35.3227	0.9541
	2000		1	8.1200	4.0600	72.4462	1.9353
	500		1	8.4400	4.2200	16.8715	0.5194
	1000	70%	1	9.0100	4.5050	35.3962	1.1790
	2000		0.9350	9.7778	4.8889	72.8293	9.7143
	500		0.5800	14.8334	7.4167	16.9897	9.5254
	1000	50%	0.2250	21.4546	10.7273	35.7115	28.9731
	2000		0.0800	17.5000	8.2500	72.4546	67.5950
GFR($J = 4$)	500		1	8.9600	2.2400	8.2202	0.3185
	1000	90%	1	9.4600	2.3650	17.3058	0.6937
	2000		1	9.7800	2.4450	35.5461	1.5884
	500		1	11.5600	2.8900	8.2217	0.4644
	1000	70%	1	12.4252	3.1063	17.3298	1.0364
	2000		0.9200	12.7112	3.1778	35.5907	5.4671
	500		0.5450	19.4544	4.8636	8.2735	5.0755
	1000	50%	0.2150	21.6000	5.4000	17.4886	14.4169
	2000		0.0900	27.6200	6.9050	35.9331	35.0428

Table 3: Simulation results of Example 1, scenario (iii).

Method	p	R^2	CP	AFP	AFN	AMS	Time3 (s)
FR	500	90%	1	0.1200	0	8.1200	1.1145
	1000		1	0.0100	0	8.0100	2.1929
	2000		1	0.0200	0	8.0200	4.4733
	500	70%	0.5750	0.0500	0.3500	7.7000	1.0480
	1000		0.4500	0.3200	1.4300	6.8900	2.0102
	2000		0.2550	0.1500	2.6900	5.4600	3.6044
	500	50%	0	0.0200	5.1400	2.8800	0.2783
	1000		0	0.0200	5.9000	2.1200	0.3805
	2000		0	0.0500	6.3600	1.6900	0.5836
GFR($J = 2$)	500	90%	1	0.0400	0	8.0400	0.4675
	1000		1	0.0800	0	8.0800	0.9451
	2000		1	0.0800	0	8.0800	1.9091
	500	70%	0.8400	0.2300	0.4500	7.7800	0.4613
	1000		0.5300	0.3000	1.5800	6.7200	0.7660
	2000		0.3900	0.5200	2.2200	6.3000	1.4399
	500	50%	0.0100	0.3500	5.8500	2.5000	0.1035
	1000		0	0.4300	6.2500	2.1800	0.1704
	2000		0	0.5200	6.3800	2.1400	0.3296
GFR($J = 4$)	500	90%	1	1.2800	0	9.2800	0.3210
	1000		1	1.7600	0	9.7600	0.6962
	2000		1	1.8400	0	9.8400	1.4139
	500	70%	0.7300	1.3400	1.4200	7.9200	0.2482
	1000		0.3700	1.3000	2.7400	6.5600	0.3740
	2000		0.2950	1.3800	4.1400	5.2400	0.5153
	500	50%	0.0100	1.4000	5.2800	4.1200	0.0804
	1000		0	1.5600	5.5200	4.0400	0.1545
	2000		0	1.9800	5.9400	4.0400	0.3090
SIS	500	90%	0.0200	23.4500	2.4500	29.0000	0.0218
	1000		0.0050	24.0250	3.0250	29.0000	0.0786
	2000		0	24.2600	3.2600	29.0000	0.2974
	500	70%	0.0100	23.7900	2.7900	29.0000	0.0219
	1000		0	24.3350	3.3350	29.0000	0.0784
	2000		0	24.6650	3.6650	29.0000	0.3004
	500	50%	0	24.3000	3.3000	29.0000	0.0248
	1000		0	24.8600	3.8600	29.0000	0.0899
	2000		0	25.3300	4.3300	29.0000	0.3269
ISIS	500	90%	1	108.0000	0	116.0000	0.0530
	1000		1	108.0000	0	116.0000	0.1321
	2000		0.9850	108.0250	0.0250	116.0000	0.4095
	500	70%	0.8900	108.1150	0.1150	116.0000	0.0509
	1000		0.6700	108.4350	0.4350	116.0000	0.1301
	2000		0.3250	109.1250	1.1250	116.0000	0.4103
	500	50%	0.3950	108.8400	0.8400	116.0000	0.0519
	1000		0.1000	109.9250	1.9250	116.0000	0.1279
	2000		0.0200	111.0350	3.0350	116.0000	0.3982

Table 4: Simulation results of Example 2, scenario (i).

p	R^2	FR		GFR($J = 2$)		GFR($J = 4$)	
		CP	Time (s)	CP	Time (s)	CP	Time (s)
500	90%	1	0.2992	1	0.3776	1	0.5104
1000		1	0.7010	1	0.8487	1	1.1190
2000		1	4.3744	1	4.6684	1	5.2827
500	70%	0.9950	0.3001	1	0.3791	1	0.5083
1000		0.9850	0.7114	0.9900	0.8485	1	1.1099
2000		0.9900	4.3898	0.9850	4.6705	0.9950	5.2033
500	50%	0.7850	0.3014	0.8400	0.3787	0.9150	0.5199
1000		0.7100	0.6925	0.8050	0.8560	0.8800	1.1349
2000		0.6950	4.3795	0.7700	4.7253	0.8350	5.2680

Table 5: Simulation results of Example 2, scenario (ii).

Method	p	R^2	CP	AMS	iter	Time1 (s)	Time2 (s)
FR	500		1	3.0000	3.0000	32.8695	0.2599
	1000	90%	1	3.0000	3.0000	69.1921	0.5219
	2000		1	3.0000	3.0000	144.6914	1.0535
	500		1	3.0050	3.0050	32.6123	0.2606
	1000	70%	0.9950	3.0101	3.0101	68.6967	0.8658
	2000		0.9950	3.0653	3.0653	145.2301	1.8179
	500		0.9500	3.8316	3.8316	32.9186	2.0148
	1000	50%	0.8500	4.0000	4.0000	69.1772	10.9656
	2000		0.7200	3.5556	3.5556	144.9864	40.2103
GFR($J = 2$)	500		1	4.0400	2.0200	16.8159	0.1746
	1000	90%	1	4.0500	2.0250	35.5480	0.3521
	2000		1	4.0500	2.0250	75.8053	0.7142
	500		1	4.1500	2.0750	16.8271	0.2146
	1000	70%	0.9950	4.1106	2.0553	35.4387	0.4281
	2000		0.9850	4.0914	2.0457	75.4025	1.4179
	500		0.9250	6.3530	3.1765	16.9038	1.9379
	1000	50%	0.8800	5.6316	2.8158	35.6034	5.0057
	2000		0.8050	4.7000	2.3500	75.8922	17.2509
GFR($J = 4$)	500		1	4.5000	1.1250	8.2943	0.0966
	1000	90%	1	4.4600	1.1150	17.5272	0.1903
	2000		1	4.4000	1.1000	38.8654	0.3771
	500		1	4.9200	1.2300	8.2625	0.1213
	1000	70%	1	4.7600	1.1900	17.3947	0.2149
	2000		0.9950	4.9696	1.2424	36.0217	0.8492
	500		0.9400	5.7192	1.4298	8.2867	0.7015
	1000	50%	0.9100	5.1620	1.2905	17.8103	1.8052
	2000		0.8850	5.5204	1.3801	39.0071	6.5094

Table 6: Simulation results of Example 2, scenario (iii).

Method	p	R^2	CP	AFP	AFN	AMS	Time3 (s)
FR	500	90%	1	0.0333	0	3.0350	0.2669
	1000		1	0.0067	0	3.0050	0.5269
	2000		1	0.0200	0	3.0200	1.0728
	500	70%	0.9950	0.0400	0.0050	3.0350	0.2652
	1000		0.9700	0.0150	0.0350	2.9800	0.5190
	2000		0.9650	0.0250	0.0350	2.9900	1.0585
	500	50%	0.5000	0.0650	0.5400	2.5250	0.2158
	1000		0.3750	0.0400	0.6750	2.3650	0.4006
	2000		0.3800	0.0350	0.6600	2.3750	0.8133
GFR($J = 2$)	500	90%	1.0000	1.0600	0	4.0600	0.1788
	1000		1.0000	1.0500	0	4.0500	0.3532
	2000		1.0000	1.0500	0	4.0500	0.7084
	500	70%	0.8200	0.9700	0.1800	3.7900	0.1643
	1000		0.8150	0.9150	0.1850	3.7300	0.3194
	2000		0.7450	0.8400	0.2600	3.5800	0.6107
	500	50%	0.2300	0.4800	0.9000	2.5800	0.1045
	1000		0.2200	0.3900	0.8700	2.5200	0.2026
	2000		0.2000	0.3500	0.8700	2.4800	0.4019
GFR($J = 4$)	500	90%	1.0000	1.5000	0	4.5000	0.0969
	1000		0.9950	1.4450	0.0050	4.4400	0.1898
	2000		1.0000	1.4000	0	4.4000	0.3745
	500	70%	0.7950	1.2900	0.2100	4.0800	0.0793
	1000		0.8300	1.3700	0.1700	4.2000	0.1698
	2000		0.7950	1.2650	0.2050	4.0600	0.3158
	500	50%	0.6300	1.3850	0.3850	4.0000	0.0760
	1000		0.6800	1.3350	0.3350	4.0000	0.1532
	2000		0.6250	1.3850	0.3850	4.0000	0.3057
SIS	500	90%	1.0000	26.0000	0	29.0000	0.0216
	1000		1.0000	26.0000	0	29.0000	0.0773
	2000		1.0000	26.0000	0	29.0000	0.4183
	500	70%	1.0000	26.0000	0	29.0000	0.0217
	1000		1.0000	26.0000	0	29.0000	0.0775
	2000		1.0000	26.0000	0	29.0000	0.4191
	500	50%	0.9950	26.0050	0.0050	29.0000	0.0222
	1000		0.9950	26.0050	0.0050	29.0000	0.0791
	2000		0.9750	26.0250	0.0250	29.0000	0.4169
ISIS	500	90%	1.0000	113.0000	0	116.0000	0.0538
	1000		1.0000	113.0000	0	116.0000	0.1347
	2000		1.0000	113.0000	0	116.0000	0.5474
	500	70%	1.0000	113.0000	0	116.0000	0.0504
	1000		1.0000	113.0000	0	116.0000	0.1334
	2000		1.0000	113.0000	0	116.0000	0.5673
	500	50%	0.9950	113.0050	0.0050	116.0000	0.0512
	1000		0.9950	113.0050	0.0050	116.0000	0.1266
	2000		0.9800	113.0200	0.0200	116.0000	0.5431

Table 7: Simulation results of Example3, scenario (i).

p	R^2	FR		GFR($J = 2$)		GFR($J = 4$)	
		CP	Time (s)	CP	Time (s)	CP	Time (s)
500	90%	0.5000	0.5973	1	0.7165	1	0.9788
1000		0.3050	1.2458	0.9950	1.4566	0.9950	2.0121
2000		0.2350	2.6009	0.9950	3.0360	0.9900	4.1696
500	70%	0.0550	0.6010	0.5850	0.7110	0.705	0.9752
1000		0.0100	1.2486	0.4300	1.4476	0.4950	1.9991
2000		0.0200	2.5964	0.3750	3.0176	0.4400	4.1575
500	50%	0.0050	0.5953	0.2200	0.7111	0.3450	0.9767
1000		0	1.2194	0.1550	1.4564	0.2000	2.0005
2000		0	2.5473	0.0700	3.0350	0.1350	4.1425

Table 8: Simulation results of Example 3, scenario (ii).

Method	p	R^2	CP	AMS	iter	Time1 (s)	Time2 (s)
FR	500		1	5.5150	5.5150	31.5283	0.6470
	1000	90%	1	5.8550	5.8550	66.4831	1.3978
	2000		1	5.8995	5.8995	136.5545	2.8402
	500		0.7250	9.1379	9.1379	31.5440	12.1350
	1000	70%	0.5350	11.9065	11.9065	66.5275	36.4303
	2000		0.4300	8.8372	8.8372	136.7187	79.8748
	500		0.2850	17.5263	17.5263	31.5433	23.3161
	1000	50%	0.1400	17.2857	17.2857	66.5714	58.3595
	2000		0.0400	17.8750	17.8750	137.4194	131.7264
GFR($J = 2$)	500		1	7.3000	3.6500	16.1349	0.4118
	1000	90%	0.9950	7.3970	3.6985	34.1177	0.8488
	2000		0.9950	7.5778	3.7889	70.1851	2.4704
	500		0.7650	12.1700	6.0850	16.1258	5.2963
	1000	70%	0.5450	12.0918	6.0459	34.0971	19.3409
	2000		0.4450	10.2022	5.1011	70.0645	43.2803
	500		0.3950	19.8228	9.9114	16.1479	11.2915
	1000	50%	0.2650	19.1320	9.5660	34.0703	26.4529
	2000		0.1350	19.1112	9.5556	70.1724	65.6157
GFR($J = 4$)	500		1	11.2800	2.8200	7.9370	0.4282
	1000	90%	1	11.5200	2.8800	16.7251	0.8762
	2000		0.9900	11.5352	2.8838	34.4208	2.1484
	500		0.7950	15.4968	3.8742	7.9275	2.4925
	1000	70%	0.5800	14.9312	3.7328	16.7046	8.5706
	2000		0.4900	14.6124	3.6531	34.3767	19.5655
	500		0.4750	20.4632	5.1158	7.9367	5.1953
	1000	50%	0.2800	18.7144	4.6786	16.7158	13.1580
	2000		0.1850	23.2432	5.8108	34.4379	30.2443

Table 9: Simulation results of Example 3, scenario (iii).

Method	p	R^2	CP	AFP	AFN	AMS	Time3 (s)
FR	500	90%	0.9650	0.5300	0.0350	5.4950	0.6673
	1000		0.9000	0.7400	0.1000	5.6400	1.3855
	2000		0.8750	0.8700	0.1250	5.7450	2.8385
	500	70%	0.1100	0.9500	0.8950	5.0550	0.5832
	1000		0.1150	1.3450	0.8850	5.4500	1.3032
	2000		0.0600	1.6650	0.9600	5.7050	2.5906
	500	50%	0.0150	1.3250	2.2550	4.0700	0.4522
	1000		0.0150	1.5000	2.8300	3.6700	0.7955
	2000		0.0050	1.3750	3.2850	3.0900	1.2730
GFR($J = 2$)	500	90%	0.7550	2.0550	0.2450	6.8100	0.3863
	1000		0.6450	2.0550	0.3550	6.7000	0.7515
	2000		0.6050	2.1850	0.3950	6.7900	1.5292
	500	70%	0.2000	1.8900	0.8000	6.0900	0.3454
	1000		0.1550	1.9800	0.8500	6.1300	0.7010
	2000		0.1150	2.0700	0.8900	6.1800	1.4215
	500	50%	0.0750	1.7300	1.4400	5.2900	0.2807
	1000		0.0400	1.6800	1.6700	5.0100	0.5192
	2000		0.0200	1.5950	2.0050	4.5900	0.9061
GFR($J = 4$)	500	90%	0.2850	4.1350	0.7150	8.4200	0.2630
	1000		0.2200	4.1200	0.7800	8.3400	0.5168
	2000		0.2050	4.1550	0.7950	8.3600	1.0404
	500	70%	0.1700	3.9050	0.9250	7.9800	0.2480
	1000		0.1300	3.8550	1.0550	7.8000	0.4766
	2000		0.1000	3.8050	1.1450	7.6600	0.9367
	500	50%	0.0900	3.3000	1.4600	6.8400	0.1922
	1000		0.0600	3.2950	1.6350	6.6600	0.3689
	2000		0.0300	3.2500	1.7500	6.5000	0.7137
SIS	500	90%	0	25.4200	1.4200	29.0000	0.0213
	1000		0	25.5600	1.5600	29.0000	0.0765
	2000		0	25.6300	1.6300	29.0000	0.2909
	500	70%	0	25.5400	1.5400	29.0000	0.0227
	1000		0	25.6750	1.6750	29.0000	0.0811
	2000		0	25.7700	1.7700	29.0000	0.3040
	500	50%	0	25.7200	1.7200	29.0000	0.0227
	1000		0	25.8750	1.8750	29.0000	0.0769
	2000		0	25.9950	1.9950	29.0000	0.3074
ISIS	500	90%	0	112.0000	1.0000	116.0000	0.0549
	1000		0	112.0150	1.0150	116.0000	0.1387
	2000		0	112.0150	1.0150	116.0000	0.4183
	500	70%	0	112.0750	1.0750	116.0000	0.0554
	1000		0	112.1900	1.1900	116.0000	0.1313
	2000		0	112.3100	1.3100	116.0000	0.4002
	500	50%	0	112.2000	1.2000	116.0000	0.0515
	1000		0	112.4300	1.4300	116.0000	0.1294
	2000		0	112.5650	1.5650	116.0000	0.4236

Table 10: Indices of selected genes for the breast cancer data.

Method	Genes
FR	272, 167, 5342
GFR($J = 2$)	272, 166
GFR($J = 4$)	272, 166, 275, 267, 24032, 11913, 11870, 17439

Table 11: Average PMSEs of different methods when applied to the breast cancer data.

SIS	ISIS	FR	GFR($J = 2$)	GFR($J = 4$)
0.4804	0.5260	0.4807	0.5081	0.4365

Table 12: Selected probes for the rats eye data.

Method	Genes
FR	1383110_at, 1389584_at, 1392692_at
GFR($J = 2$)	1383110_at, 1389584_at, 1392692_at, 1378099_at
GFR($J = 4$)	1383110_at, 1389584_at, 1383673_at, 1386683_at

Table 13: Average PMSEs of different methods when applied to the rats eye data.

SIS	ISIS	FR	GFR($J = 2$)	GFR($J = 4$)
0.6291	0.8502	0.6948	0.6592	0.6026